

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/578,562  
Source: IFWP  
Date Processed by STIC: 5/18/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 05/18/2006

PATENT APPLICATION: US/10/578,562

TIME: 09:42:50

Input Set : A:\39702a.txt

Output Set: N:\CRF4\05182006\J578562.raw

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3 <110> APPLICANT: Weaver et al.
5 <120> TITLE OF INVENTION: METHODS OF TREATING CHRONIC PAIN USING COMPOSITIONS THAT
6 SPECIFICALLY BIND CD11D (ALPHA-D) INTEGRIN
8 <130> FILE REFERENCE: 27866/39702
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/578,562
C--> 10 <141> CURRENT FILING DATE: 2006-05-08
10 <160> NUMBER OF SEQ ID NOS: 2
12 <170> SOFTWARE: PatentIn version 3.1
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 3726
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (3)..(3485)
22 <223> OTHER INFORMATION:
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27 Thr Phe Gly Thr Val Leu Leu Leu Ser Val Leu Ala Ser Tyr His
28 1 5 10 15
30 gga ttc aac ctg gat gtg gag gag cct acg atc ttc cag gag gat gca 95
31 Gly Phe Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala
32 20 25 30
34 ggc ggc ttt ggg cag agc gtg gtg cag ttc ggt gga tct cga ctc gtg 143
35 Gly Gly Phe Gly Gln Ser Val Val Gln Phe Gly Gly Ser Arg Leu Val
36 35 40 45
38 gtg gga gca ccc ctg gag gtg gtg gcg gcc aac cag acg gga cgg ctg 191
39 Val Gly Ala Pro Leu Glu Val Val Ala Ala Asn Gln Thr Gly Arg Leu
40 50 55 60
42 tat gac tgc gca gct gcc acc ggc atg tgc cag ccc atc ccg ctg cac 239
43 Tyr Asp Cys Ala Ala Ala Thr Gly Met Cys Gln Pro Ile Pro Leu His
44 65 70 75
46 atc cgc cct gag gcc gtg aac atg tcc ttg ggc ctg acc ctg gca gcc 287
47 Ile Arg Pro Glu Ala Val Asn Met Ser Leu Gly Leu Thr Leu Ala Ala
48 80 85 90 95
50 tcc acc aac ggc tcc cgg ctc ctg gcc tgt ggc ccg acc ctg cac aga 335
51 Ser Thr Asn Gly Ser Arg Leu Leu Ala Cys Gly Pro Thr Leu His Arg
52 100 105 110
54 gtc tgt ggg gag aac tca tac tca aag ggt tcc tgc ctc ctg ctg ggc 383
55 Val Cys Gly Glu Asn Ser Tyr Ser Lys Gly Ser Cys Leu Leu Leu Gly
56 115 120 125
58 tcg cgc tgg gag atc atc cag aca gtc ccc gac gcc acg cca gag tgt 431
59 Ser Arg Trp Glu Ile Ile Gln Thr Val Pro Asp Ala Thr Pro Glu Cys

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60	130	135	140	
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65	Pro His Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser			
66	145	150	155	
68	att gac caa aat gac ttt aac cag atg aag ggc ttt gtc caa gct gtc	527		
69	Ile Asp Gln Asn Asp Phe Asn Gln Met Lys Gly Phe Val Gln Ala Val			
70	160	165	170	175
72	atg ggc cag ttt gag ggc act gac acc ctg ttt gca ctg atg cag tac	575		
73	Met Gly Gln Phe Glu Gly Thr Asp Thr Leu Phe Ala Leu Met Gln Tyr			
74	180	185	190	
76	tca aac ctc ctg aag atc cac ttc acc ttc acc caa ttc cgg acc agc	623		
77	Ser Asn Leu Leu Lys Ile His Phe Thr Phe Thr Gln Phe Arg Thr Ser			
78	195	200	205	
80	ccg agc cag cag agc ctg gtg gat ccc atc gtc caa ctg aaa ggc ctg	671		
81	Pro Ser Gln Gln Ser Leu Val Asp Pro Ile Val Gln Leu Lys Gly Leu			
82	210	215	220	
84	acg ttc acg gcc acg ggc atc ctg aca gtg gtg aca cag cta ttt cat	719		
85	Thr Phe Thr Ala Thr Gly Ile Leu Thr Val Val Thr Gln Leu Phe His			
86	225	230	235	
88	cat aag aat ggg gcc cga aaa agt gcc aag aag atc ctc att gtc atc	767		
89	His Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile Val Ile			
90	240	245	250	255
92	aca gat ggg cag aag tac aaa gac ccc ctg gaa tac agt gat gtc atc	815		
93	Thr Asp Gly Gln Lys Tyr Lys Asp Pro Leu Glu Tyr Ser Asp Val Ile			
94	260	265	270	
96	ccc cag gca gag aag gct ggc atc atc cgc tac gct atc ggg gtg gga	863		
97	Pro Gln Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly			
98	275	280	285	
100	cac gct ttc cag gga ccc act gcc agg cag gag ctg aat acc atc agc	911		
101	His Ala Phe Gln Gly Pro Thr Ala Arg Gln Glu Leu Asn Thr Ile Ser			
102	290	295	300	
104	tca gcg cct ccg cag gac cac gtg ttc aag gtg gac aac ttt gca gcc	959		
105	Ser Ala Pro Pro Gln Asp His Val Phe Lys Val Asp Asn Phe Ala Ala			
106	305	310	315	
108	ctt ggc agc atc cag aag cag ctg cag gag aag atc tat gca gtt gag	1007		
109	Leu Gly Ser Ile Gln Lys Gln Leu Gln Glu Lys Ile Tyr Ala Val Glu			
110	320	325	330	335
112	gga acc cag tcc agg gca agc agc tcc ttc cag cac gag atg tcc caa	1055		
113	Gly Thr Gln Ser Arg Ala Ser Ser Ser Phe Gln His Glu Met Ser Gln			
114	340	345	350	
116	gaa ggc ttc agc aca gcc ctc aca atg gat ggc ctc ttc ctg ggg gct	1103		
117	Glu Gly Phe Ser Thr Ala Leu Thr Met Asp Gly Leu Phe Leu Gly Ala			
118	355	360	365	
120	gtg ggg agc ttt agc tgg tct gga ggt gcc ttc ctg tat ccc cca aat	1151		
121	Val Gly Ser Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro Asn			
122	370	375	380	
124	atg agc ccc acc ttc atc aac atg tct cag gag aat gtg gac atg agg	1199		
125	Met Ser Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met Arg			
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128	gac	tct	tac	ctg	ggt	tac	tcc	acc	gag	cta	gcc	ctg	tgg	aag	ggg	gta	1247
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130	400					405					410					415	
132	cag	aac	ctg	gtc	ctg	ggg	gcc	ccc	cgc	tac	cag	cat	acc	ggg	aag	gct	1295
133	Gln	Asn	Leu	Val	Leu	Gly	Ala	Pro	Arg	Tyr	Gln	His	Thr	Gly	Lys	Ala	
134					420					425					430		
136	gtc	atc	ttc	acc	cag	gtg	tcc	agg	caa	tgg	agg	aag	aag	gcc	gaa	gtc	1343
137	Val	Ile	Phe	Thr	Gln	Val	Ser	Arg	Gln	Trp	Arg	Lys	Lys	Ala	Glu	Val	
138				435						440					445		
140	aca	ggg	acg	cag	atc	ggc	tcc	tac	ttc	ggg	gcc	tcc	ctc	tgc	tcc	gtg	1391
141	Thr	Gly	Thr	Gln	Ile	Gly	Ser	Tyr	Phe	Gly	Ala	Ser	Leu	Cys	Ser	Val	
142			450					455					460				
144	gat	gtg	gac	agc	gat	ggc	agc	acc	gac	ctg	atc	ctc	att	ggg	gcc	ccc	1439
145	Asp	Val	Asp	Ser	Asp	Gly	Ser	Thr	Asp	Leu	Ile	Leu	Ile	Gly	Ala	Pro	
146		465					470					475					
148	cat	tac	tat	gag	cag	acc	cga	ggg	ggc	cag	gtg	tcc	gtg	tgt	ccc	ttg	1487
149	His	Tyr	Tyr	Glu	Gln	Thr	Arg	Gly	Gly	Gln	Val	Ser	Val	Cys	Pro	Leu	
150	480					485				490					495		
152	cct	agg	ggg	cag	agg	gtg	cag	tgg	cag	tgt	gac	gct	gtt	ctc	cgt	ggg	1535
153	Pro	Arg	Gly	Gln	Arg	Val	Gln	Trp	Gln	Cys	Asp	Ala	Val	Leu	Arg	Gly	
154					500					505					510		
156	gag	cag	ggc	cac	ccc	tgg	ggc	cgc	ttt	ggg	gca	gcc	ctg	aca	gtg	ttg	1583
157	Glu	Gln	Gly	His	Pro	Trp	Gly	Arg	Phe	Gly	Ala	Ala	Leu	Thr	Val	Leu	
158				515					520					525			
160	ggg	gat	gtg	aat	gag	gac	aag	ctg	ata	gac	gtg	gcc	att	ggg	gcc	ccg	1631
161	Gly	Asp	Val	Asn	Glu	Asp	Lys	Leu	Ile	Asp	Val	Ala	Ile	Gly	Ala	Pro	
162			530					535					540				
165	gga	gag	cag	gag	aac	cgg	ggt	gct	gtc	tac	ctg	ttt	cac	gga	gcc	tca	1679
166	Gly	Glu	Gln	Glu	Asn	Arg	Gly	Ala	Val	Tyr	Leu	Phe	His	Gly	Ala	Ser	
167		545					550					555					
169	gaa	tcc	ggc	atc	agc	ccc	tcc	cac	agc	cag	cgg	att	gcc	agc	tcc	cag	1727
170	Glu	Ser	Gly	Ile	Ser	Pro	Ser	His	Ser	Gln	Arg	Ile	Ala	Ser	Ser	Gln	
171	560					565				570					575		
173	ctc	tcc	ccc	agg	ctg	cag	tat	ttt	ggg	cag	gcg	ctg	agt	ggg	ggg	cag	1775
174	Leu	Ser	Pro	Arg	Leu	Gln	Tyr	Phe	Gly	Gln	Ala	Leu	Ser	Gly	Gly	Gln	
175					580					585					590		
177	gac	ctc	acc	cag	gat	gga	ctg	atg	gac	ctg	gcc	gtg	ggg	gcc	cgg	ggc	1823
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179				595				600					605				
181	cag	gtg	ctc	ctg	ctc	agg	agt	ctg	ccg	gtg	ctg	aaa	gtg	ggg	gtg	gcc	1871
182	Gln	Val	Leu	Leu	Leu	Arg	Ser	Leu	Pro	Val	Leu	Lys	Val	Gly	Val	Ala	
183			610					615					620				
185	atg	aga	ttc	agc	cct	gtg	gag	gtg	gcc	aag	gct	gtg	tac	cgg	tgc	tgg	1919
186	Met	Arg	Phe	Ser	Pro	Val	Glu	Val	Ala	Lys	Ala	Val	Tyr	Arg	Cys	Trp	
187		625					630					635					
191	gaa	gag	aag	ccc	agt	gcc	ctg	gaa	gct	ggg	gac	gcc	acc	gtc	tgt	ctc	1967
192	Glu	Glu	Lys	Pro	Ser	Ala	Leu	Glu	Ala	Gly	Asp	Ala	Thr	Val	Cys	Leu	
193	640					645				650					655		
195	acc	atc	cag	aaa	agc	tca	ctg	gac	cag	cta	ggt	gac	atc	caa	agc	tct	2015

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201				675					680					685			
203	att	ttc	aat	gaa	acc	aag	aac	ccc	act	ttg	act	cga	aga	aaa	acc	ctg	2111
204	Ile	Phe	Asn	Glu	Thr	Lys	Asn	Pro	Thr	Leu	Thr	Arg	Arg	Lys	Thr	Leu	
205			690					695					700				
207	gga	ctg	ggg	att	cac	tgt	gaa	acc	ctg	aag	ctg	ctt	ttg	cca	gat	tgt	2159
208	Gly	Leu	Gly	Ile	His	Cys	Glu	Thr	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Cys	
209		705					710					715					
211	gtg	gag	gat	gtg	gtg	agc	ccc	atc	att	ctg	cac	ctc	aac	ttc	tca	ctg	2207
212	Val	Glu	Asp	Val	Val	Ser	Pro	Ile	Ile	Leu	His	Leu	Asn	Phe	Ser	Leu	
213	720					725					730					735	
215	gtg	aga	gag	ccc	atc	ccc	tcc	ccc	cag	aac	ctg	cgt	cct	gtg	ctg	gcc	2255
216	Val	Arg	Glu	Pro	Ile	Pro	Ser	Pro	Gln	Asn	Leu	Arg	Pro	Val	Leu	Ala	
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219	gtg	ggc	tca	caa	gac	ctc	ttc	act	gct	tct	ctc	ccc	ttc	gag	aag	aac	2303
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221				755					760					765			
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225			770					775					780				
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229	Phe	Ser	Gly	Leu	Gln	Thr	Leu	Thr	Val	Gly	Ser	Ser	Leu	Glu	Leu	Asn	
230		785					790					795					
232	gtg	att	gtg	act	gtg	tgg	aac	gca	ggg	gag	gat	tcc	tac	gga	acc	gtg	2447
233	Val	Ile	Val	Thr	Val	Trp	Asn	Ala	Gly	Glu	Asp	Ser	Tyr	Gly	Thr	Val	
234	800					805					810					815	
236	gtc	agc	ctc	tac	tat	cca	gca	ggg	ctg	tgc	cac	cga	cgg	gtg	tca	gga	2495
237	Val	Ser	Leu	Tyr	Tyr	Pro	Ala	Gly	Leu	Ser	His	Arg	Arg	Val	Ser	Gly	
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240	gcc	cag	aag	cag	ccc	cat	cag	agt	gcc	ctg	cgc	ctg	gca	tgt	gag	aca	2543
241	Ala	Gln	Lys	Gln	Pro	His	Gln	Ser	Ala	Leu	Arg	Leu	Ala	Cys	Glu	Thr	
242				835					840					845			
244	gtg	ccc	act	gag	gat	gag	ggc	cta	aga	agc	agc	cgc	tgc	agt	gtc	aac	2591
245	Val	Pro	Thr	Glu	Asp	Glu	Gly	Leu	Arg	Ser	Ser	Arg	Cys	Ser	Val	Asn	
246			850					855					860				
248	cac	ccc	atc	ttc	cat	gag	ggc	tct	aac	ggc	acc	ttc	ata	gtc	aca	ttc	2639
249	His	Pro	Ile	Phe	His	Glu	Gly	Ser	Asn	Gly	Thr	Phe	Ile	Val	Thr	Phe	
250		865					870					875					
254	gat	gtc	tcc	tac	aag	gcc	acc	ctg	gga	gac	agg	atg	ctt	atg	agg	gcc	2687
255	Asp	Val	Ser	Tyr	Lys	Ala	Thr	Leu	Gly	Asp	Arg	Met	Leu	Met	Arg	Ala	
256	880					885					890					895	
258	agt	gca	agc	agt	gag	aac	aat	aag	gct	tca	agc	agc	aag	gcc	acc	ttc	2735
259	Ser	Ala	Ser	Ser	Glu	Asn	Asn	Lys	Ala	Ser	Ser	Ser	Lys	Ala	Thr	Phe	
260				900							905				910		
262	cag	ctg	gag	ctc	ccg	gtg	aag	tat	gca	gtc	tac	acc	atg	atc	agc	agg	2783
263	Gln	Leu	Glu	Leu	Pro	Val	Lys	Tyr	Ala	Val	Tyr	Thr	Met	Ile	Ser	Arg	

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268		930		935		940		
270	aaa atg aaa gag gct gag cat cga tac cgt gtg aat aac ctc agc cag							2879
271	Lys Met Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Gln							
272		945		950		955		
274	cga gat ctg gcc atc agc att aac ttc tgg gtt cct gtc ctg ctg aac							2927
275	Arg Asp Leu Ala Ile Ser Ile Asn Phe Trp Val Pro Val Leu Leu Asn							
276	960		965		970		975	
278	ggg gtg gct gtg tgg gat gtg gtc atg gag gcc cca tct cag agt ctc							2975
279	Gly Val Ala Val Trp Asp Val Val Met Glu Ala Pro Ser Gln Ser Leu							
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282	ccc tgt gtt tca gag aga aaa cct ccc cag cat tct gac ttc ctg acc							3023
283	Pro Cys Val Ser Glu Arg Lys Pro Pro Gln His Ser Asp Phe Leu Thr							
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286	cag att tca aga agt ccc atg ctg gac tgc tcc att gct gac tgc							3068
287	Gln Ile Ser Arg Ser Pro Met Leu Asp Cys Ser Ile Ala Asp Cys							
288		1010		1015		1020		
291	ctg cag ttc cgc tgt gac gtc ccc tcc ttc agc gtc cag gag gag							3113
292	Leu Gln Phe Arg Cys Asp Val Pro Ser Phe Ser Val Gln Glu Glu							
293		1025		1030		1035		
295	ctg gat ttc acc ctg aag ggc aat ctc agt ttc ggc tgg gtc cgc							3158
296	Leu Asp Phe Thr Leu Lys Gly Asn Leu Ser Phe Gly Trp Val Arg							
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299	gag aca ttg cag aag aag gtg ttg gtc gtg agt gtg gct gaa att							3203
300	Glu Thr Leu Gln Lys Lys Val Leu Val Val Ser Val Ala Glu Ile							
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303	acg ttc gac aca tcc gtg tac tcc cag ctt cca gga cag gag gca							3248
304	Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala							
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308	Phe Met Arg Ala Gln Met Glu Met Val Leu Glu Glu Asp Glu Val							
309		1085		1090		1095		
311	tac aat gcc att ccc atc atc atg ggc agc tct gtg ggg gct ctg							3338
312	Tyr Asn Ala Ile Pro Ile Ile Met Gly Ser Ser Val Gly Ala Leu							
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317	cta ctg ctg gcg ctc atc aca gcc aca ctg tac aag ctt ggc ttc							3383
318	Leu Leu Leu Ala Leu Ile Thr Ala Thr Leu Tyr Lys Leu Gly Phe							
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321	ttc aaa cgc cac tac aag gaa atg ctg gag gac aag cct gaa gac							3428
322	Phe Lys Arg His Tyr Lys Glu Met Leu Glu Asp Lys Pro Glu Asp							
323		1130		1135		1140		
325	act gcc aca ttc agt ggg gac gat ttc agc tgt gtg gcc cca aat							3473
326	Thr Ala Thr Phe Ser Gly Asp Asp Phe Ser Cys Val Ala Pro Asn							
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329	gtg cct ttg tcc taataatcca ctttctgtt tatctctacc actgtgggct							3525
330	Val Pro Leu Ser							
331		1160						

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:25 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:22